IN THE SPECIFICATION:

Page 18, please replace the paragraph beginning on line 6 with the following rewritten paragraph:

Stratagene provided a genomic Hyacinth Macaw Lambda FixII Library (Cat. No. 946402). Plaques were screened at moderate stringency with a 1.3Kb Chicken *CHD-W* subclone (spans 2670-4003 nucleotides in the related Mouse CHD1 gene (Delmas *et al.*, 1993)). A *CHD-W* genomic fragment was isolated and aligned to the chicken and mouse homologues to allow the design and construction of 3 primers (5' to 3')
P3 AGATATTCCGGATCTGATAGTGA (SEQ ID NO: 38),
P2 TCTGCATCGCTAAATCCTTT (SEQ ID NO: 39) and
P1ATATTCTGGATCTGATAGTGA(C/T)TC (SEQ ID NO: 37).

Page 19, please replace the paragraph beginning on line 20 with the following rewritten paragraph:

All the birds listed above were sexed from DNA using exactly the same PCR reaction. PCR reaction volumes of 20 µl were made up of Promega Taq buffer (1x is 50mM KCl, 10mM Tris.HCl, 1.5 mM $MgCl_2$, 0.1% Triton X-100), 200 µM of each dNTP, P2 (5'-TCTGCATCGCTAAATCCTTT) (SEQ ID NO: 39) and P3 (5'-AGATATTCCGGATCTGATAGTGA) (SEQ ID NO: 38) primers (approx 1 µM), 50-200 ng of genomic DNA and 0.15 units of Taq polymerase. The thermal treatment was 94 °C/1.5 mins followed by 30 cycles of 55 or 56 °C/15 sec, 72 °C/15 sec, and 94 °C/30 sec with a finish of 56 °C/1 min and 72 °C/5 min. *HaeIII* (5 units; Promega) was used to cut 8 µl if PCR product in 1x Promega restriction enzyme buffer 3 and 50 ng/µl bovine serum albumin (Sigma) in a total volume of 10 µl. The digests and uncut PCR product were precipitated before being electrophoresed in a visigel (Stratagene) with ethidium bromide (40 ng/ml) at 3.5 V/cm.

Page 29, please replace the paragraph beginning on line 21 with the following rewritten paragraph:

The *HaeIII* restriction enzyme cut the *CHD-1A* fragment alone in all 3 ~~13~~ species (Fig 17) and, from the sequence data, would also have worked on the Spix's Macaw (Fig 16). Figure 17 shows that the *CHD-1A* in males is cut into two fragments (45bp, 59bp) which are not easily visible on the gel. In females *CHD-W* is uncut by *HaeIII* so remains at 104bp. The discrimination using *HaeIII* provided correct sex identification in all individuals.

Page 32, please replace the paragraph beginning on line 22 with the following rewritten paragraph:

The second functional domain was identified by Delmas *et al.* (1993) as having sequence selective DNA binding capacity. Whether this is highly specific or just A+T rich regions was not established. They also noted that this domain contains Lys-Arg-Pro-Lys-Lys (SEQ ID NO: 40) and Arg-Gly-Arg-Pro-Arg (SEQ ID NO: 41) motifs which enable genes like *HMG-1*, *D1* and *Engrailed* to bind in the minor groove of A+T rich DNA.